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## SEQUENCE LISTING

&lt;110&gt; LUDWIG INSTITUTE FOR CANCER RESEARCH

<120> TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND  
OF A NEW UBIQUITOUSLY EXPRESSED GENE

&lt;130&gt; L0461/7034WO

&lt;150&gt; US 60/085,318

&lt;151&gt; 1998-05-13

&lt;160&gt; 11

&lt;170&gt; FastSEQ for Window Version 3.0

&lt;210&gt; 1

&lt;211&gt; 1382

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 738..989

&lt;400&gt; 1

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ttttctcctc tggtgacaat atagtgtcca acacttgga gtagattttta agaattgttta      180
tttaaattaa aaggatggat ttccaaggaa aaaaaataag gaaaaggaaa gaaaaaactg      240
aacagaaaac gcaaaagtat cagtttggtc actaaccttt gcaaggatac ctttttatatt      300
tctttaagat tcctgttgtt tatacacaga ttttaagttt actcctactg ctgaccecaag      360
tgaaattcct tctccagtca cagtgtcaac ctctaccccc caactgcaac gagagttttg      420
aggggcatca atcacaccga gaagtcacag cccctcaacc actgaggtgt gggggggtag      480
ggatctgcat ttcttcatat caaccccaca ctatagggca cctaaatggg tgggcgggtg      540
gggagaccga ctcacttgag tttcttgaag gcttcctggc ctccagccac gtaattgccc      600
ccgctctgga tctggtctag cttccggatt cgggtggccag tccgcggggt gtagatgttc      660
ctgacggccc caaagggtgc ctgaacgccg ccggtcacct ccttcaggaa gacttcgaag      720
ctggacacct tcttctc atg gat gac gac gcg gcg ccc cgc gta gaa ggg      770
                Met Asp Asp Asp Ala Ala Pro Arg Val Glu Gly
                        1             5             10
gtc ccc gtt gcg gta cac aag cac gct ctt cac gac ggg ctg aga cag      818
Val Pro Val Ala Val His Lys His Ala Leu His Asp Gly Leu Arg Gln
                        15             20             25
gtg gct gga cct ggc gct gct gcc gct cat ctt ccc cgc tgg ccg ccg      866
Val Ala Gly Pro Gly Ala Ala Ala Ala His Leu Pro Arg Trp Pro Pro
                        30             35             40
cct cag ctc gct gct tcg cgt cgg gag gca cct ccg ctg tcc cag cgg      914
Pro Gln Leu Ala Ala Ser Arg Arg Glu Ala Pro Pro Leu Ser Gln Arg
                        45             50             55
cct cac cgc acc cag ggc gcg gga tcg cct cct gaa acg aac gag aaa      962
Pro His Arg Thr Gln Gly Ala Gly Ser Pro Pro Glu Thr Asn Glu Lys
60                        65                        70                        75
ctg acg aat cca cag gtg aaa gag aag taacggccgt gcgcctaggc gtccacc      1016
Leu Thr Asn Pro Gln Val Lys Glu Lys

```

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cagaggagac actaggagct tgcaggactc ggagtagacg ctcaagtttt tcaccgtggc 1076
gtgcacagcc aatcaggacc cgcagtgcgc gcaccacacc aggttcacct gctacgggca 1136
gaatcaaggt ggacagcttc tgagcaggag ccggaaacgc gcggggcctt caaacaggca 1196
cgcctagtga gggcaggaga gaggaggacg cacacacaca cacacacaca aatatggtga 1256
aacccaattt cttacatcat atctgtgcta ccttttccaa acagcctaata ttttcttttc 1316
tctcttcttg cacctttacc cctcaatctc ctgcttcctc ccaaattaaa gcaattaagt 1376
tcctgg 1382

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<210> 2
<211> 84
<212> PRT
<213> Homo sapiens

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His Lys His Ala Leu His Asp Gly Leu Arg Gln Val Ala Gly Pro Gly
20          25          30
Ala Ala Ala Ala His Leu Pro Arg Trp Pro Pro Pro Gln Leu Ala Ala
35          40          45
Ser Arg Arg Glu Ala Pro Pro Leu Ser Gln Arg Pro His Arg Thr Gln
50          55          60
Gly Ala Gly Ser Pro Pro Glu Thr Asn Glu Lys Leu Thr Asn Pro Gln
65          70          75          80
Val Lys Glu Lys

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<210> 3
<211> 9
<212> PRT
<213> Homo sapiens

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<400> 3
Leu Pro Arg Trp Pro Pro Pro Gln Leu
1          5

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<210> 4
<211> 2167
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 303..1730

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<400> 4
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gattggctgt gcacgccacg gtgaaaaact tgagcgtcta ctccgagtc tgcaagctcc 120
tagtgtctcc tctgggtgga cgcctaggcg cagggccgtt acttctcttt cacctgtgga 180
ttcgtcagtt tctcgttcgt ttcaggaggc gateccgcgc cctgggtgcg gtgagggcgc 240
tgggacagcg gaggtgctc ccgacgcgaa gcagcgagct gaggcggcgg ccagcgggga 300
ag atg agc ggc agc agc gcc agg tcc agc cac ctg tct cag ccc gtc 347
Met Ser Gly Ser Ser Ala Arg Ser Ser His Leu Ser Gln Pro Val
1          5          10          15
gtg aag agc gtg ctt gtg tac cgc aac ggg gac ccc ttc tac gcg ggg 395
Val Lys Ser Val Leu Val Tyr Arg Asn Gly Asp Pro Phe Tyr Ala Gly
20          25          30
cgc cgc gtc gtc atc cat gag aag aag gtg tcc agc ttc gaa gtc ttc 443

```

PCT/US99/10424

Arg	Arg	Val	Val	Ile	His	Glu	Lys	Lys	Val	Ser	Ser	Phe	Glu	Val	Phe	
			35					40					45			
ctg	aag	gag	gtg	acc	ggc	ggc	gtt	cag	gca	ccc	ttt	ggg	gcc	gtc	agg	491
Leu	Lys	Glu	Val	Thr	Gly	Gly	Val	Gln	Ala	Pro	Phe	Gly	Ala	Val	Arg	
		50					55					60				
aac	atc	tac	acc	ccg	cgg	act	ggc	cac	cga	atc	cgg	aag	cta	gac	cag	539
Asn	Ile	Tyr	Thr	Pro	Arg	Thr	Gly	His	Arg	Ile	Arg	Lys	Leu	Asp	Gln	
		65					70					75				
atc	cag	agc	ggg	ggc	aat	tac	gtg	gct	gga	ggc	cag	gaa	gcc	ttc	aag	587
Ile	Gln	Ser	Gly	Gly	Asn	Tyr	Val	Ala	Gly	Gly	Gln	Glu	Ala	Phe	Lys	
80					85					90					95	
aaa	ctc	aat	tac	ttg	gac	ata	gga	gaa	atc	aag	aaa	aga	cca	atg	gaa	635
Lys	Leu	Asn	Tyr	Leu	Asp	Ile	Gly	Glu	Ile	Lys	Lys	Arg	Pro	Met	Glu	
				100					105					110		
gtt	gtt	aat	aca	gag	gta	aaa	cca	gta	atc	cat	agc	agg	atc	aac	gtg	683
Val	Val	Asn	Thr	Glu	Val	Lys	Pro	Val	Ile	His	Ser	Arg	Ile	Asn	Val	
			115					120					125			
tca	gct	cgc	ttt	aga	aaa	ccg	ctt	cag	gag	ccg	tgc	act	atc	ttc	ttg	731
Ser	Ala	Arg	Phe	Arg	Lys	Pro	Leu	Gln	Glu	Pro	Cys	Thr	Ile	Phe	Leu	
		130					135					140				
att	gca	aat	gga	gac	ctc	ata	aac	cca	gct	tct	cgc	ctc	ctt	atc	ccc	779
Ile	Ala	Asn	Gly	Asp	Leu	Ile	Asn	Pro	Ala	Ser	Arg	Leu	Leu	Ile	Pro	
		145					150				155					
aga	aaa	acc	ttg	aat	cag	tgg	gat	cat	gta	cta	caa	atg	gtc	aca	gaa	827
Arg	Lys	Thr	Leu	Asn	Gln	Trp	Asp	His	Val	Leu	Gln	Met	Val	Thr	Glu	
160					165				170						175	
aaa	atc	act	ctg	agg	agc	ggg	gct	gtt	cac	agg	ctt	tat	act	tta	gaa	875
Lys	Ile	Thr	Leu	Arg	Ser	Gly	Ala	Val	His	Arg	Leu	Tyr	Thr	Leu	Glu	
				180					185					190		
gga	aaa	ctt	gtt	gag	agt	gga	gca	gag	ttg	gag	aat	ggg	cag	ttt	tat	923
Gly	Lys	Leu	Val	Glu	Ser	Gly	Ala	Glu	Leu	Glu	Asn	Gly	Gln	Phe	Tyr	
			195					200					205			
gtg	gct	gtt	ggc	aga	gat	aag	ttt	aag	aaa	ctg	cct	tac	ggg	gag	tta	971
Val	Ala	Val	Gly	Arg	Asp	Lys	Phe	Lys	Lys	Leu	Pro	Tyr	Gly	Glu	Leu	
		210					215					220				
ctt	ttt	gac	aag	tca	acg	atg	aga	agg	cct	ttt	ggg	cag	aaa	gct	tct	1019
Leu	Phe	Asp	Lys	Ser	Thr	Met	Arg	Arg	Pro	Phe	Gly	Gln	Lys	Ala	Ser	
		225				230					235					
tca	cta	cct	cct	att	gta	gga	tcc	aga	aag	tct	aaa	ggg	agt	gga	aat	1067
Ser	Leu	Pro														

- 4 -

Glu Val Pro Val Asp Gln Arg Pro Ala Glu Ile Val Asp Glu Glu Glu  
 340 345 350  
 gat gga gag aag gca aac aag gat gca gaa cag aaa gaa gac ttt tca 1403  
 Asp Gly Glu Lys Ala Asn Lys Asp Ala Glu Gln Lys Glu Asp Phe Ser  
 355 360 365  
 gga atg aat ggt gac ctt gaa gag gaa gga ggt agg gag gct aca gat 1451  
 Gly Met Asn Gly Asp Leu Glu Glu Gly Gly Arg Glu Ala Thr Asp  
 370 375 380  
 gcc cct gag caa gtc gag gag att ctg gat cac agt gag cag cag gca 1499  
 Ala Pro Glu Gln Val Glu Glu Ile Leu Asp His Ser Glu Gln Gln Ala  
 385 390 395  
 cgc cct gct cgt gta aat gga ggc acc gat gag gag aat ggt gag gag 1547  
 Arg Pro Ala Arg Val Asn Gly Gly Thr Asp Glu Glu Asn Gly Glu Glu  
 400 405 410 415  
 ctg cag cag gtt aat aat gag ctt caa ctg gtc cta gac aag gaa aga 1595  
 Leu Gln Gln Val Asn Asn Glu Leu Gln Leu Val Leu Asp Lys Glu Arg  
 420 425 430  
 aag tct caa gga gct ggc agt gga caa gat gag gct gat gta gac cct 1643  
 Lys Ser Gln Gly Ala Gly Ser Gly Gln Asp Glu Ala Asp Val Asp Pro  
 435 440 445  
 caa aga cca cca agg cca gaa gta aaa att acc agt cca gaa gaa aat 1691  
 Gln Arg Pro Pro Arg Pro Glu Val Lys Ile Thr Ser Pro Glu Glu Asn  
 450 455 460  
 gaa aac aac caa caa aac aag gac tat gct gcc gtg gct tagaagattt tt 1742  
 Glu Asn Asn Gln Gln Asn Lys Asp Tyr Ala Ala Val Ala  
 465 470 475  
 aaaaagagag tatatggatc gcaagaaaaa tgaagggtta tcatacttga aagataagca 1802  
 catagttatt gctgaatata atgtgacact atggtcgaat actacctacg aattataaca 1862  
 ttagaagcct agtggaaaga ccagataact ttaaattggct actaaaggat aattacttac 1922  
 ttttattgca tgtgttttaa aagtcatata gaaatattaa ataagacgga cagaggagaa 1982  
 tttgcaactgg aagacaattg ccacttgtaa aggatgaaaa ataggatcac tcttattgta 2042  
 cgctttatta taagtttaga aggcagttta ttctaaataa tttttctcta ggaaggcgta 2102  
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 gaatg 2167

&lt;210&gt; 5

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

Met Ser Gly Ser Ser Ala Arg Ser Ser His Leu Ser Gln Pro Val Val  
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 Lys Ser Val Leu Val Tyr Arg Asn Gly Asp Pro Phe Tyr Ala Gly Arg  
 20 25 30  
 Arg Val Val Ile His Glu Lys Lys Val Ser Ser Phe Glu Val Phe Leu  
 35 40 45  
 Lys Glu Val Thr Gly Gly Val Gln Ala Pro Phe Gly Ala Val Arg Asn  
 50 55 60  
 Ile Tyr Thr Pro Arg Thr Gly His Arg Ile Arg Lys Leu Asp Gln Ile  
 65 70 75 80  
 Gln Ser Gly Gly Asn Tyr Val Ala Gly Gly Gln Glu Ala Phe Lys Lys  
 85 90 95  
 Leu Asn Tyr Leu Asp Ile Gly Glu Ile Lys Lys Arg Pro Met Glu Val  
 100 105 110  
 Val Asn Thr Glu Val Lys Pro Val Ile His Ser Arg Ile Asn Val Ser  
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<210> 6
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<212> DNA
<213> Homo sapiens
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18

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<211> 18
<212> DNA
<213> Homo sapiens
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 <400> 8  
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 <210> 10  
 <211> 246  
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 <213> Homo sapiens  
  
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 agattttaag tttactccta ctgctgaccc aagtgaatt ccttctccag tcacagtgtc 120  
 aacctctacc cccaactgc aacgagagtt ttgaggggca tcaatcacac cgagaagtca 180  
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 acacta 246  
  
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 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
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 <222> 242..242  
 <223> n = a, c, g or t  
  
 <220>  
 <221> unsure  
 <222> 317..317  
 <223> n = a, c, g or t  
  
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 <222> 320..320  
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- 7 -

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<400> 11

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60

"H4030" e037.360

- 8 -

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ggcgtagaat	tttaaagaac	tggtaatagg	aaagcatgta	ctatttttctt	aaagcaataa	180
actcttgaat	gaacagattg	cgattttactt	tcagacataa	tttggagatg	gcagtagatc	240
anaatgtgtc	catgacttgt	taacatgcct	ttccgttctt	cctccttaag	ccaaaatcca	300
ccttttgact	acaaatnccn	gagcaaggcg	ttcattttttg	gtgggaagga	agcattgggt	360
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ccngttanag	tttataaagc	ctggatggta	tggttngccg	agtaatgnga	aatcctgtgg	540
gantttccac	tgatccaggt	ccaatcttta	cccagtagnt	atctctctcc	ntctccctta	600
tgttattggg	gaa					613

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